- iii. inactivation of the lgtA gene in each strain resulting in expression of a shortened or truncated lipooligosaccharides (LOS) that lacks lacto-N-neotetraose tetrasaccharide, and
- iv. insertion of at least one second antigenically different porA gene in place of the opa gene.
- 15. The vaccine composition of claim 14, wherein the genetically modified strain further comprises increased or stable expression of at least one minor conserved outer membrane protein.
- 16. The vaccine composition of claim 14, wherein the genetically modified strain further comprises stabilized expression of at least one outer membrane protein, wherein the outer membrane protein is selected from the group comprising Opc and PorA.
- 17. The vaccine composition of claim 14, wherein the at least one second antigenically different porA gene expresses at least one PorA subtype protein or subtype epitope selected from the most prevalent of PorA subtypes of meningitidis group  $\beta$  isolates.
- 18. The vaccine composition of claim 15, wherein the at least one minor conserved outer membrane protein is selected from the group consisting of: FHBP (GNA1870) variants 1, FHBP variant 2, FHBP variant 3; NadA; App, NspA, TbpA and B.
- **19**. A genetically modified vaccine strain of *Neisseria meningitidis* subtype B strain: comprising H44/76 HOPS-D strain.
- **20**. The genetically modified vaccine strain of *Neisseria meningitidis* subtype B of claim **19**, wherein the strain is derived from: H44/76 strain comprising the genetic modifications of
  - i) inactivation of a synX gene,
  - ii) inactivation of the lpxL1 gene,
  - iii) inactivation of the lgtA gene,
  - iv) insertion of a second porA gene in the place of a opaD gene,
  - v) increased expression of NadA compared with the native strain, and
  - vi) stabilized increased expression of Opc and PorA proteins.
- 21. The genetically modified strain of claim 19, wherein strain H44/76 HOPS-DL was derived from the ET-5 wild type strain H44/76 (B:15: P1.7,16: L,3,7:P5.5,C).
- **22**. A genetically modified vaccine strain of *Neisseria meningitidis* subtype B comprising strain: 8570 HOS-G1.
- 23. The genetically modified vaccine strain of *Neisseria* meningitidis subtype B strain of claim 22, wherein the strain is derived from 8570 comprising the genetic modifications of:
  - i) inactivation of a synX gene,
  - ii) inactivation of the lpxL1 gene,
  - iii) inactivation of the lgtA gene,
  - iv) insertion of a second porA gene in place of opaD;
  - v) increased expression of factor H binding protein variant 1: and
  - vi) stabilized increased expression of PorA and Opc proteins
- **24**. The genetically modified strain of claim **22**, wherein the genetically modified strain was derived from the ET-5 wild type strain 85 70(B:4: P1.19,15: L3,7v: P5.5,11,C).
- **25**. A genetically modified vaccine strain of *Neisseria meningitidis* subtype B comprising B16B6 HPS-G<sub>2</sub>A strain.

- **26**. The genetically modified vaccine strain of *Neisseria meningitidis* subtype B of claim **25**, wherein the strain is derived from B16B6 comprising the genetic modifications of:
  - i) inactivation of a synX gene,
  - ii) inactivation of the lpxL1 gene,
  - iii) inactivation of the lgtA gene,
  - iv) insertion of a second porA gene (subtype P1.22-1,4) in place of opaD;
  - v) increased expression of factor H binding protein variant 2: and
  - vi) stabilized increased expression of PorA and Opc proteins.
- 27. The genetically modified strain of claim 25, wherein the genetically modified strain is derived from the ET-37 wild type strain B16B6 (B:2a:P1.5,2: L2:P5.1,2,5).
- **28**. The genetically modified strain of claim **19**, wherein the strain is grown in iron deficient medium
- 29. The genetically modified strain of claim 20, wherein inactivation of synX gene, lpxL1 gene, or lgtA gene is by an insertion of a drug resistance gene within the sequence of the inactivated gene.
- **30**. A vaccine composition comprising NOMV from one or more genetically modified strain of *Neisseria meningitidis* subtype B selected from the group consisting of:
  - a) genetically modified vaccine strain of *Neisseria meningitidis* subtype B derived from: H44/76 strain comprising the genetic modifications of
    - i) inactivation of a synX gene,
      - ii) inactivation of the lpxL1 gene,
      - iii) inactivation of the lgtA gene,
      - iv) insertion of a second porA gene in the place of a opaD gene.
      - v) increased expression of NadA compared with the native strain, and
      - vi) stabilized increased expression of Opc and PorA proteins;
  - b) a genetically modified vaccine strain of *Neisseria meningitidis* subtype B strain derived from 8570 comprising the genetic modifications of:
    - i) inactivation of a synX gene,
    - ii) inactivation of the lpxL1 gene,
    - iii) inactivation of the lgtA gene,
    - iv) insertion of a second porA gene in place of opaD;
    - v) increased expression of factor H binding protein variant 1; and
    - vi) stabilized increased expression of PorA and Opc proteins; and
  - c) a genetically modified vaccine strain of *Neisseria meningitidis* subtype B derived from B16B6 comprising the genetic modifications of:
    - i) inactivation of a synX gene,
    - ii) inactivation of the lpxL1 gene,
    - iii) inactivation of the lgtA gene,
    - iv) insertion of a second porA gene (subtype P1.22-1,4) in place of opaD;
    - v) increased expression of factor H binding protein variant 2; and
    - vi) stabilized increased expression of PorA and Opc proteins.
- **31**. The vaccine composition of claim **30**, wherein the vaccine composition comprises NOMVs from two or more genetically modified strains.
  - 32. (canceled)